#7

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<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer P64-1

<400> 17
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<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer 64-4

<400> 18
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<210> 19
<211> 840
<212> DNA
<213> Artificial Sequence

<220> Feature
<221> Nucleotide substitutions.
<222> Position 536
<223> At position 536 "n" denotes a or g or c or t/u
<223> Description of Artificial Sequence:
oligonucleotide 80d

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Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg
    370                 375                 380

ggg gaa gaa tcg atc aag gac tct tac cgc tgc cgt cgc cgg aag gtg   1200
Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val
385                 390                 395                 400

gtc gac ccg tcc gca cct ggg cag cac gaa ggc acg tgc aac gtc agc   1248
Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser
                405                 410                 415

atg gcg gca ctc gac aag ttc gtt gcg gaa cgc atc ttc aac aag atc   1296
Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile
            420                 425                 430

agg cac gcc gaa ggc gac gaa gag acg ttg gcg ctt ctg tgg gaa gcc   1344
Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala
        435                 440                 445

gcc cga cgc ttc ggc aag ctc act gag gcg cct gag aag agc ggc gaa   1392
Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu
    450                 455                 460

cgg gcg aac ctt gtt gcg gag cgc gcc gac gcc ctg aac gcc ctt gaa   1440
Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu
465                 470                 475                 480

gag ctg tac gaa gac cgc gcg gca ggc gcg tac gac gga ccc gtt ggc   1488
Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly
                485                 490                 495

agg aag cac ttc cgg aag caa cag gca gcg ctg acg ctc cgg cag caa   1536
Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln
            500                 505                 510

ggg gcg gaa gag cgg ctt gcc gaa ctt gaa gcc gcc gaa gcc ccg aag   1584
Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys
        515                 520                 525

ctt ccc ctt gac caa tgg ttc ccc gaa gac gcc gac gct gac ccg acc   1632
Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr
    530                 535                 540

ggc cct aag tcg tgg tgg ggg cgc gcg tca gta gac gac aag cgc gtg   1680
Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val
545                 550                 555                 560

ttc gtc ggg ctc ttc gta gac aag atc gtt gtc acg aag tcg act acg   1728
Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr
                565                 570                 575

ggc agg ggg cag gga acg ccc atc gag aag cgc gct tcg atc acg tgg   1776
Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp
            580                 585                 590

gcg aag ccg ccg acc gac gac gac gaa gac gac gcc cag gac ggc acg   1824
Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr
        595                 600                 605

gaa gac gta gcg gcg cct aag aag aag agg aag gtt tag               1863
Glu Asp Val Ala Ala Pro Lys Lys Lys Arg Lys Val
    610                 615                 620
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<210> 23
<211> 620
<212> DNA

<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: DNA sequence
encoding the fusion protein C31-Int(CNLS)
<400> 23

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            20                  25                  30

Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu
        35                  40                  45

Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu
    50                  55                  60

Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu
65                  70                  75                  80

Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val
                85                  90                  95

Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro
            100                 105                 110

Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln
        115                 120                 125

Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile
    130                 135                 140

Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys
145                 150                 155                 160

Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly
                165                 170                 175

Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile
            180                 185                 190

Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His
        195                 200                 205

Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile
    210                 215                 220

Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys
225                 230                 235                 240

Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys
                245                 250                 255

Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly
            260                 265                 270

Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile
        275                 280                 285

Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys
    290                 295                 300

Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile
305                 310                 315                 320

Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro
                325                 330                 335
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